

Figure 1

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GGCATGGGCACTCGGGGTCACTCCTCCTGCTCGGCTCCTTACGGCGGCAGCGGGCGGCGG 120
A W A I A V I I L P R I I T A A A A A A
GGCGGTGACGTACGGGGTGATGTACAGTGTCTGCCATGACCTGGAGACGGTGGAGGT 180
A V T S R G D V T V V C H D L E T V E V
CACGTGGGGCTCGGGCCCCGACCACCACGGCGCCAACTTGAGCCTGGAGTTCCGTTATGG 240
T W G S G P D H H G A N L S L E F R Y G
TACTGGGGCCCTGCAACCCTGCCCGGATATTTCTGTCCGGCGCTGGTGTCACTTCGGG 300
T G A L Q P C P R Y F L S G A G V T S G
GTGCATCCTCCCCCGGCGAGGGCGGGGCTGCTGGAGCTGGCACTGCGCGACGGAGGCGG 360
C I L P A A R A G L L E L A L R D G G G
GGCATGGTGTTAAGGCTAGGCAGCGCGCTCCGCTGGCTGAAGCCCCGCCACCTTG 420
A M V F K A R Q R A S A W L K P R P P W
GAATGTGACGCTGCTCTGGACACCAGACGGGGACGTGACTGTCTCCTGGCCTGCCCACTC 480
N V T L L W T P D G D V T V S W P A H S
CTACCTGGGCCTGGACTACGAGGTGCAGCACCGGGAGAGCAATGACGATGAGGACGCCCTG 540
Y L G L D Y E V Q H R E S N D D E D A W
GCAGACGACCTCAGGGCCCTGCTGTGACTTGACAGTGGGGCGGGCTCGACCCCGCGCGCTG 600
Q T T S G P C C D L T V G G L D P A R C
CTATGACTTCCGGGTTCGGGCGTCCGCCCGGGCGCGCACTATGGCCTGGAGGCGCAGCC 660
Y D F R V R A S P R A A H Y G L E A Q P
TAGCGAGTGGACAGCGGTGACAAGGCTTTCCGGGGCAGCATCCGCGGCCTCCTGTACCGC 720
S E W T A V T R L S G A A S A A S C T A
AAGCCCCGCCCATCCCCGGCCCTGGCCCCGGCCCTCCTGCCCTGGGCTGCGGCCTAGC 780
S P A P S P A L A P P L L P L G C G L A
AGCGCTGCTGACACTGTCCCTGCTCCTGCGCGCCCTGAGGCTTCGCAGGGTGAAAGATGC 840
A L L T L S L L L A A L R L R R V K D A
GCTGCTGCCCTGCGTCCCTGACCCAGCGGCTCCTTCCCTGGACTCTTTGAGAAGCATCA 900
L L P C V P D P S G S F P G L F E K H H
CGGGAACCTCCAGGCCTGGATTGCGGACGCCCAGGGCACAGCCCCGCCAGCCAGGACCGA 960
G N F Q A W I A D A Q A T A P P A R T E
GGAGGAAGATGACCTCATCCACCCCAAGGCTAAGAGGGTGGAGCCCGAGGACGGCACCTC 1020
E E D D L I H F K A E R V E P E D G T S
CCTCTGCACCGTGCCAAGGGCACCCAGCTTGAGGCAAGGGGGCGGGAGGCGGGGCCAT 1080
L C T V P R P P S F E P R G F G G G A M
GGTGTCACTGGGCGGGGGCACGTTTCATGGTGGGCGACAGCGGCTACATGACCTGTGAcc 1140
V S V G G A T F M V G D S G Y M T L *
ttgaagtcactgcagctctatacttcaggttgaggtcacttcctgtcttttaataattca 1200
aactcacaatacctgtgcctgtctgtatgcaaatgtgggtcagaatattcaataaaaatg 1260
caaatgctatgctaaaaa 1278

Figure 1

A

Delta1: MAWALAVILLPRLLTAAAAAAVTSRG 27

mγ_C: MLKLLSPRSFLVLQLLLLRAGWSSAVLMSSANEDIKADLIITSTAFEHLSAPTLP 58

Delta1: DVTVVCHDLETVEVTWCSGPDHGGANLSLEFRY---GTGALQPCPRYFLSGAGVTSQIL 84
+V ++E + TW S + NL+L +RY Q Q Y S +TSGQ +

mγ_C: EVQCFVFNIEYMNCTWNSSEPOATNLTLYRYKVSDNNTFQDSHYLFS-KEITSGQOI 117

Delta1: PAARAGLLELALRDGGGAMVFKARQRASAWLE-----PRPPWNVTLLWTPDGDVTVSWP 138
+ L + K ++RA L PR P N+TL + + + W

mγ_C: QKEDIQLYQTFVVLQDPQ--KPQRRVQKLNQNLVIPRAPENLTLSNLSESQLELRWK 175

Delta1: AHSYLG--LDYEVQHRESNDDELAWQTTSGPCCDLTVGGDLPARCYDFRVRASPRAAHYG 196
+ L Y VQ+R SN D - ++ +D + Y FRVR+ G

mγ_C: SKHIKERCLQYLQYR- SNRDRSWTELIVNHEPRFSLPSVDELKRYTFFVRSRYNPI-CG 233

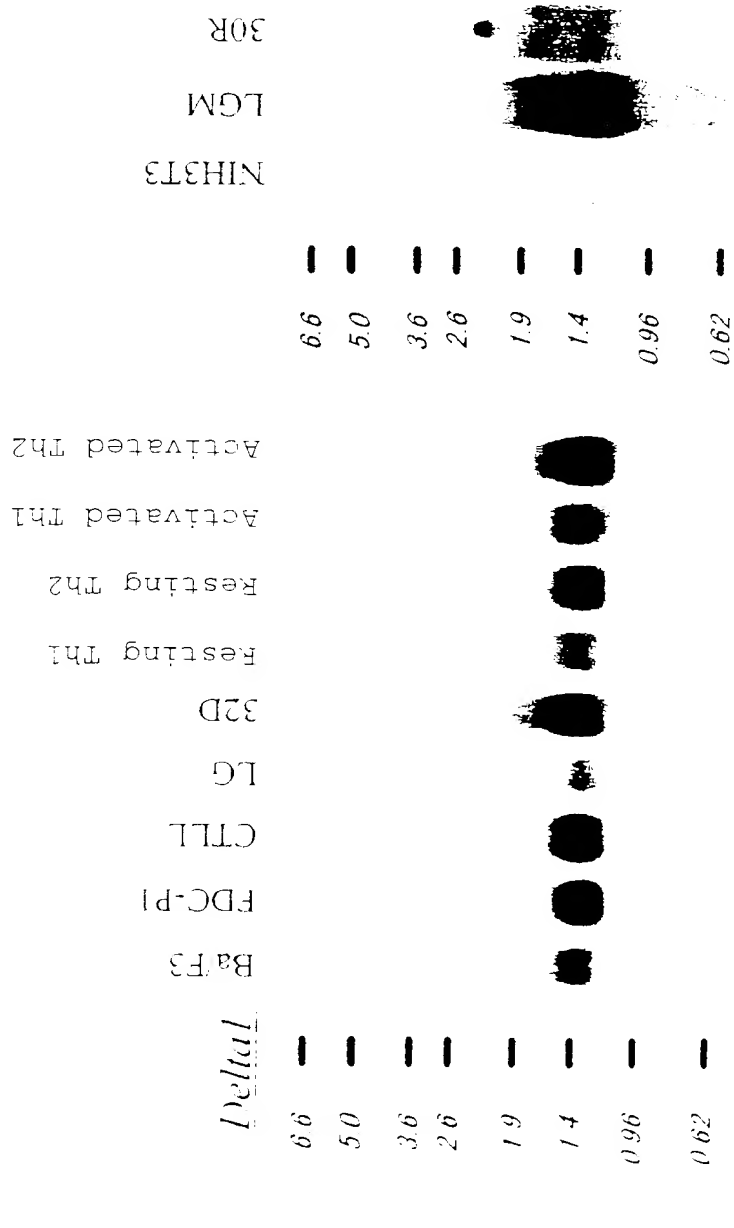
Delta1: LEAQPSEWIAVTRLGAASAASCTASPAPSPALA 230
Q S+W+

mγ_C: SSQQWSKWSQPVHWGSHTVEEN 255

B

Delta1	LLPCVPDPSCSFPGLFEKHGNGFQAWIA (19AA)	PKAKRVEPEDGTSIDCT
	: * : * : * * * * * * * * * * :	: *
mEPOR	IWPGIPSPSEFEGLFTTHKGNFQLWLL (16AA)	DPPAHLEVLSEPRWAV
	* : * * * * * * * * * * :	* : * * * *
mIL-2RB	LKCHIPDPSEFFSQLSSQHGGDLQKWLS (14AA)	PEISPLEVLDGDSKAV
	: * * * * * * *	: * * *
mγp130	IWPNVDPSPKSHIAQ-----WSP (20AA)	TDVSVVEIEANNKIPC
	: * * * * *	: * * :
AIC2B	WKEKIPNPSKSLLFQDGKGL----WPP (34AA)	NNVSPLTIEDPNIRV

Box1 region Conserved tryptophan Box1 region



β -actin

Figure 3

Heart	
Brain	
Spleen	
Lung	
Liver	
Skeletal muscle	
Kidney	
Testis	

Delta

9.5	-
7.5	-
4.4	-
2.4	-
1.35	-



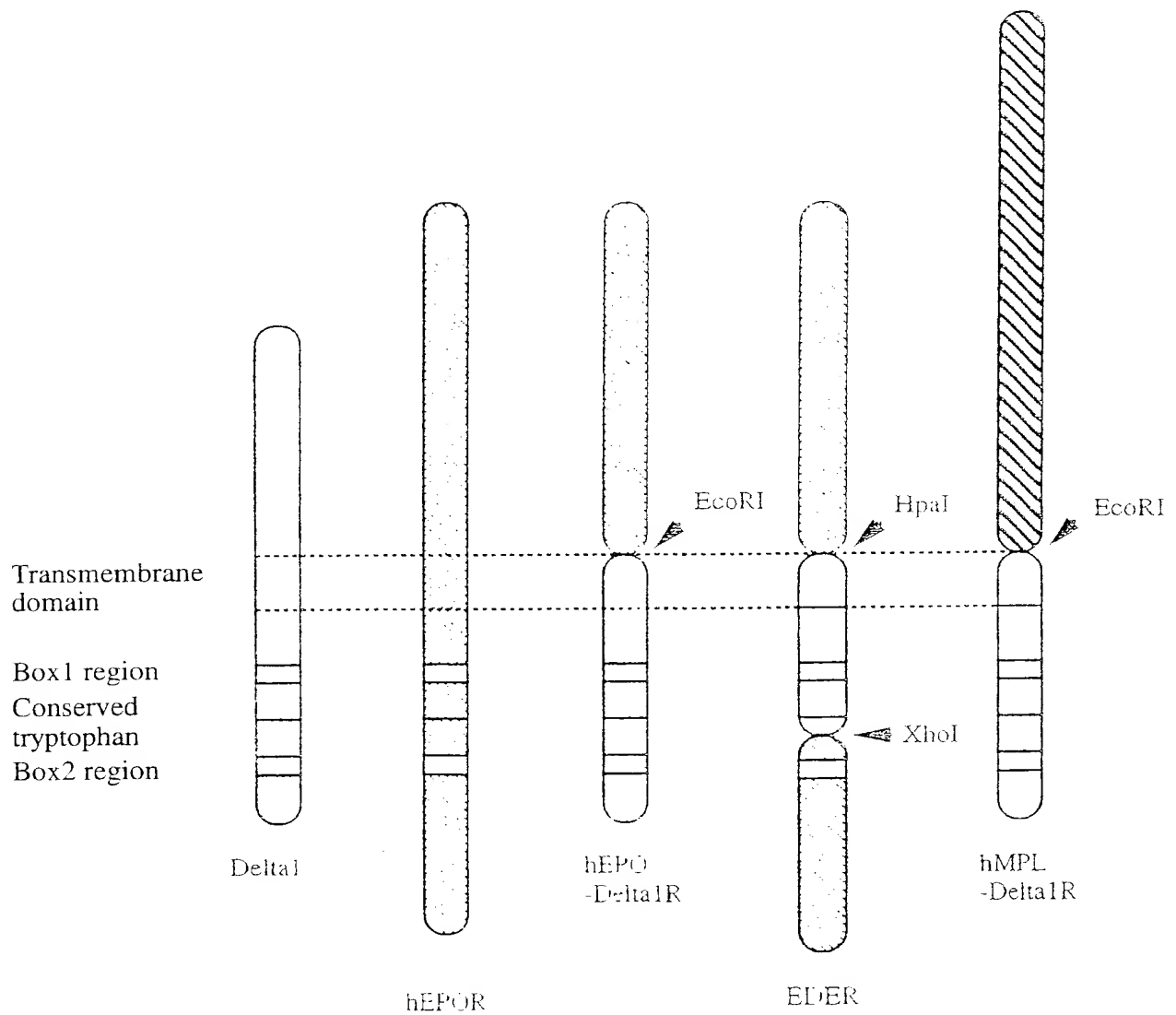
β -actin

2.4	-
1.35	-



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Figure 5



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Figure 6

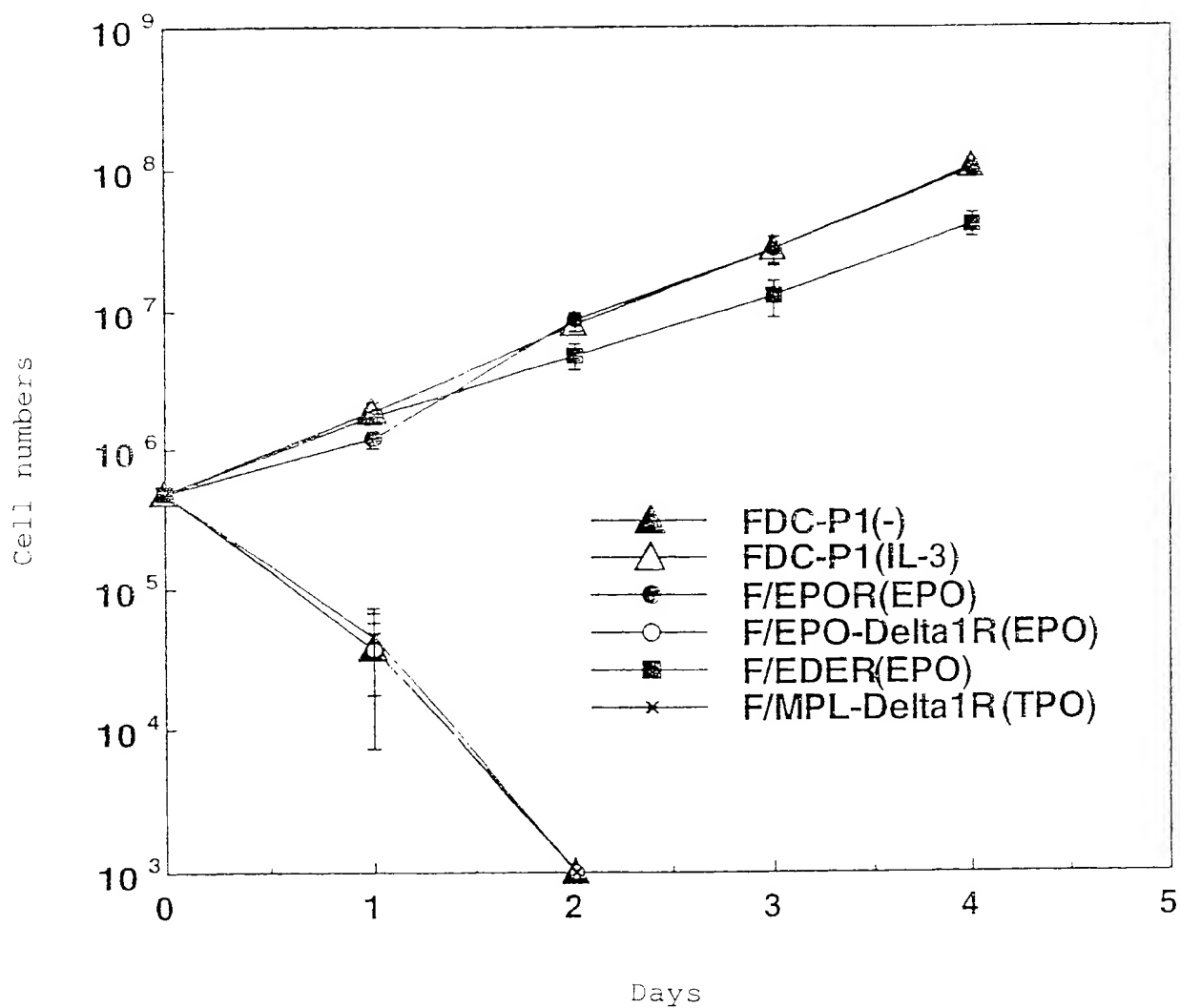
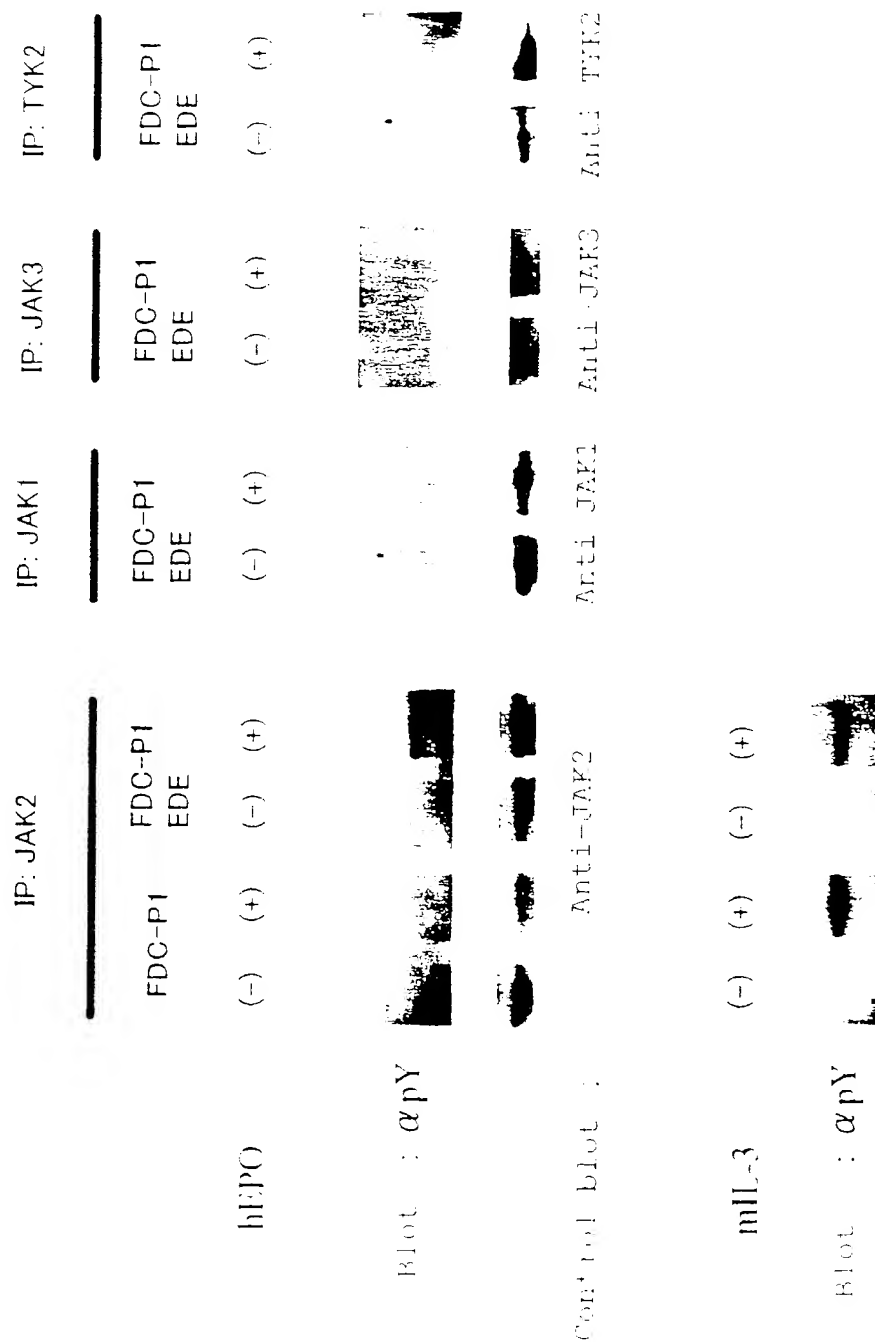
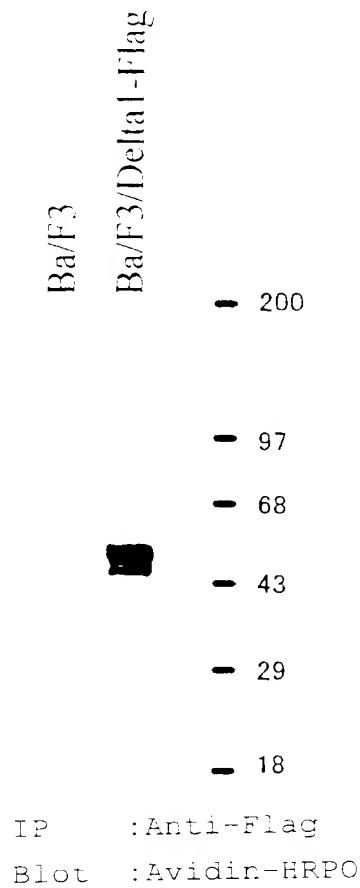


Figure 1



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Figure 6



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Figure 9

